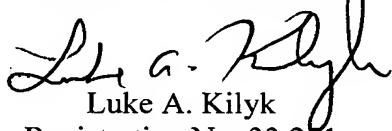


**REMARKS**

No questions of new matter are raised by the above amendment. Entry of the above amendment is therefore respectfully requested.

If there are any fees due in connection with the filing of this response, please charge the fees to deposit Account No. 50-0925. If a fee is required for an extension of time under 37 C.F.R. § 1.136 not accounted for above, such extension is requested and should also be charged to our Deposit Account.

Respectfully submitted,



Luke A. Kilyk

Registration No. 33,251

Attorney Docket No. 3900-015  
KILYK & BOWERSOX, P.L.L.C.  
53A Lee Street  
Warrenton, VA 20186  
(540) 428-1701

**VERSION WITH MARKINGS TO SHOW CHANGES MADE**

**IN THE SPECIFICATION:**

The amplification of the mutant fragments was carried out using synthesized DNA primers containing mutation sequences and a high fidelity DNA polymerase (KOD Dash, Toyobo Co., Japan), and the amplified fragments were purified by the agarose electrophoresis, phosphorylated, self-ligated, and transformed in *Escherichia coli*. Substitution of the nucleotide was confirmed by DNA-sequencing. Deletion and substitution of the spiral part of stem loop III was carried out by the fusion PCR (Virology 214, 611-618 (1995)). A forward primer (GGTAAATTCCGAGGTAAAAAATTGCTATA) containing nt6029-6050 and nt6062-6080 of PSIV sequence and a reverse primer containing nt27-5 of pT7Blue (Novagen, Inc.) were synthesized for the initial amplification to delete nucleotide (nt) 6051-6061. Then, a reverse primer (CCTCGAAATTTAACCAGATCACATAGTCAGCTTC) containing nt6043-6029 and nt6017-5998 of PSIV sequence and a forward primer containing nt28-47 of pT7Blue (Novagen, Inc.) were synthesized for another initial amplification to delete nt6028-6018. Underlines of these primers indicate 15nt overlap of the fusion PCR. After each initial amplification using these two primer sets, two amplified DNA fragments were mixed and fused according to the description in Ref. 17. The final amplification was carried out using primers carrying nt28-47 and nt27-5 of pT7Blue, and the amplified DNA fragments were purified with a gel, phosphorylated, and ligated. The initial amplification was carried out using longer primers containing a substituted nucleotide to substitute the helical part.

**IN THE CLAIMS:**

1. (Amended) An RNA higher-order structure having a function for promoting a translation activity which comprises [is made up of] a base sequence selected from the group consisting of[;]:

- 1) a base sequence expressed by sequences designated in Sequence Nos. 1 to 7 of the sequence list;
- 2) a base sequence containing the base sequence of 1);
- 3) a base sequence that has [in] at least about 50% of homology in sequence to the base sequence of 1) and that has a function for promoting a translation activity;
- 4) a complementary strand of the base sequences of 1) to 3);
- 5) a base sequence hybridizing with the base sequences of 1) to 4) under stringent conditions; and
- 6) a base sequence that has been mutated by deletion, substitution, addition, or insertion of one or more base(s) in the base sequences of 1) to 5) and that has a function for promoting a translation activity.

3. (Amended) A recombinant vector containing a polynucleotide that [is made up of any one of base sequences] comprises at least one base sequence having an RNA higher-order structure having a function for promoting a translation activity which comprises [is made up of] a base sequence selected from the group consisting of[;]:

- 1) a base sequence expressed by sequences designated in Sequence Nos. 1 to 7 of the sequence list;
- 2) a base sequence containing the base sequence of 1);

- 3) a base sequence that has at least about 50% of homology in sequence to the base sequence of 1) and that has a function for promoting a translation activity;
- 4) a complementary strand of the base sequences of 1) to 3);
- 5) a base sequence hybridizing with the base sequences of 1) to 4) under stringent conditions; and
- 6) a base sequence that has been mutated by deletion, substitution, addition, or insertion of one or more base(s) in the base sequences of 1) to 5) and that has a function for promoting a translation activity.

4. (Amended) A transformant that has been transformed with [the] a recombinant vector containing a polynucleotide that is made up of [any] one [of] or more base sequences having a higher order structure [according to claim 1 or 2.] having a function for promoting a translation activity, the sequence including a base sequence selected from:

- 1) a base sequence expressed by sequences designated in Sequence Nos. 1 to 7 of the sequence list;
- 2) a base sequence containing the base sequence of 1);
- 3) a base sequence that has at least about 50% of homology in sequence to the base sequence of 1) and that has a function for promoting a translation activity;
- 4) a complementary strand of the base sequences of 1) to 3);
- 5) a base sequence hybridizing with the base sequences of 1) to 4) under stringent conditions; and

6) a base sequence that has been mutated by deletion, substitution, addition, or insertion of one or more base(s) in the base sequences of 1) to 5) and that has a function for promoting a translation activity.

5. (Amended) A method for synthesizing a heterologous protein or a heterologous polypeptide utilizing a polynucleotide that is made up of [any] one or more [of] base sequences having an RNA higher-order structure having a function for promoting a translation activity, [which is made up of] the base sequence including a base sequence selected from the group consisting of:

- 1) a base sequence expressed by sequences designated in Sequence Nos. 1 to 7 of the sequence list;
- 2) a base sequence containing the base sequence of 1);
- 3) a base sequence that has at least about 50% of homology in sequence to the base sequence of 1) and that has a function for promoting a translation activity;
- 4) a complementary strand of the base sequences of 1) to 3);
- 5) a base sequence hybridizing with the base sequences of 1) to 4) under stringent conditions; and
- 6) a base sequence that has been mutated by deletion, substitution, addition, or insertion of one or more base(s) in the base sequences of 1) to 5) and that has a function for promoting a translation activity.

6. (Amended) [The] A method for synthesizing a heterologous protein or heterologous polypeptide [according to claim 5 wherein] utilizing a recombinant vector

containing a polynucleotide that is made up of [any] one [of] or more base sequences having a higher-order structure [according to claim 1 or 2, or transformant which has been transformed with the recombinant vector.] having a function for promoting a translation activity, the sequence including a base sequence selected from:

- 1) a base sequence expressed by sequences designated in Sequence Nos. 1 to 7 of the sequence list;
- 2) a base sequence containing the base sequence of 1);
- 3) a base sequence that has at least about 50% of homology in sequence to the base sequence of 1) and that has a function for promoting a translation activity;
- 4) a complementary strand of the base sequences of 1) to 3);
- 5) a base sequence hybridizing with the base sequences of 1) to 4) under stringent conditions; and
- 6) a base sequence that has been mutated by deletion, substitution, addition, or insertion of one or more base(s) in the base sequences of 1) to 5) and that has a function for promoting a translation activity.

7. (Amended) A method for synthesizing [or] a heterologous protein or a heterologous polypeptide [according to claim 5, wherein the synthesis is carries using the vector according to claim 6] in a cell-free protein synthesis system[.] wherein, synthesis is carried out using a recombinant vector containing a polynucleotide that is made up of one or more base sequences having a higher-order structure having a function for promoting a translation activity, the sequence including a base sequence selected from:

- 1) a base sequence expressed by sequences designated in Sequence Nos. 1 to 7 of the sequence list;
- 2) a base sequence containing the base sequence of 1);
- 3) a base sequence that has at least about 50% of homology in sequence to the base sequence of 1) and that has a function for promoting a translation activity;
- 4) a complementary strand of the base sequences of 1) to 3);
- 5) a base sequence hybridizing with the base sequences of 1) to 4) under stringent conditions; and
- 6) a base sequence that has been mutated by deletion, substitution, addition, or insertion of one or more base(s) in the base sequences of 1) to 5) and that has a function for promoting a translation activity.

9. (Amended) The method for synthesizing a heterologous protein or a heterologous polypeptide according to claim 5 [any one of claims 5 to 8], wherein the synthesis is carried out without using AUG translation initiation codon.

10. (Amended) A method for initiating synthesis of arbitrary heterologous protein or heterologous polypeptide from arbitrary codon which comprises the step[s] of changing a combination of base pairs that make up [or] PK (pseudoknot) I, II, and III structures in a RNA high-order structure having a function for promoting a translation activity, [which is made up of] the sequence including a base sequence selected from [the group consisting of]:

- 1) a base sequence expressed by sequences designated in Sequence Nos. 1 to 7 of the sequence list;

- 2) a base sequence containing the base sequence of 1);
- 3) a base sequence that has at least about 50% of homology in sequence to the base sequence of 1) and that has a function for promoting a translation activity;
- 4) a complementary strand of the base sequences of 1) to 3);
- 5) a base sequence hybridizing with the base sequences of 1) to 4) under stringent conditions; and
- 6) a base sequence that has been mutated by deletion, substitution, addition, or insertion of one or more base(s) in the base sequences of 1) to 5) and that has a function for promoting a translation activity.

11. (Amended) The method for initiating the synthesis according to claim 10 wherein, one or more combination(s) of base pairs that make up PK I is changed, and a base pair maintained in the changed higher-order structure is utilized for said initiating synthesis of said arbitrary heterologous protein or said heterologous polypeptide from said arbitrary codon.